

B. Whitman

15/108
10/11/01
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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,546A
DATE: 10/05/2001
TIME: 13:27:19

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3 <110> APPLICANT: WALLACH, David
4 GOLTSEV, Yura
5 KOVALENKO, Andrei
6 VARFOLOMEEV, Eugene
7 BRODIANSKI, Vadim
9 <120> TITLE OF INVENTION: CASH (CASPASE HOMOLOGUE) WITH DEATH EFFECTOR DOMAIN,
10 MODULATORS OF THE FUNCTION OF FAS RECEPTORS
12 <130> FILE REFERENCE: WALLACH=23
14 <140> CURRENT APPLICATION NUMBER: 09/380,546A
15 <141> CURRENT FILING DATE: 1999-11-29
17 <150> PRIOR APPLICATION NUMBER: PCT/IL98/00098
18 <151> PRIOR FILING DATE: 1998-02-26
20 <150> PRIOR APPLICATION NUMBER: IL 120367
21 <151> PRIOR FILING DATE: 1997-03-03
23 <150> PRIOR APPLICATION NUMBER: IL120759
24 <151> PRIOR FILING DATE: 1997-05-01
26 <160> NUMBER OF SEQ ID NOS: 20
28 <170> SOFTWARE: PatentIn Ver. 2.0
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32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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36 <221> NAME/KEY: CDS
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44 cacagtgaat gccggctatt ggacttttgc ccagtgcagc ctgagacaac aaggaccacg 180
46 ggaggtgagtg tagggagagaa gcgcccgcgaa cagcgatcgc ccagcaccaa gtccgcttcc 240
48 aggttttcggt tttctttgcc tccatcttgg gtgcgccttc ccggcgtota ggggagcgaa 300
50 ggctgaggtg gcagcggcag gagagtccgg ccgcgacagg acgaactccc cactggaaa 360
52 ggattctgaa agaaatgaag tcagccctca gaaatgaagt tgactgcctg ctggctttcc 420
54 tgttgactgg cccggagctg tactgcaaga cccttgtagg cttccctagt ctaagagtag 480
56 g atg tct gct gaa gtc atc cat cag gtt gaa gaa gca ctt gat aca gat 529
57 Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp
58 1 5 10 15
60 gag aag gag atg ctg ctc ttt ttg tgc cgg gat gtt gct ata gat gtg 577
61 Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
62 20 25 30
64 gtt cca cct aat gtc agg gac ctt ctg gat att tta cgg gaa aga ggt 625
65 Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
66 35 40 45
68 aag ctg tct gtc ggg gac ttg gct gaa ctg ctc tac aga gtg agg cga 673
69 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
70 50 55 60
72 ttt gac ctg ctc aaa cgt atc ttg aag atg gac aga aaa gct gtg gag 721

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77 Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
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80 atg gca gag att ggt gag gat ttg gat aaa tct gat gtg tcc tca tta 817
81 Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu
82 100 105 110
84 att ttc ctc atg aag gat tac atg ggc cga ggc aag ata agc aag gag 865
85 Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
86 115 120 125
88 aag agt ttc ttg gac ctt gtg gtt gag ttg gag aaa cta aat ttg gtt 913
89 Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
90 130 135 140
92 gcc cca gat caa ctg gat tta tta gaa aaa tgc cta aag aac atc cac 961
93 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
94 145 150 155 160
96 aga ata gac ctg aag aca aaa atc cag aag tac aag cag tct gtt caa 1009
97 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
98 165 170 175
100 gga gca ggg aca agt tac agg aat gtt ctc caa gca gca atc caa aag 1057
101 Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
102 180 185 190
104 agt ctc aag gat cct tca aat aac ttc agg ctc cat aat ggg aga agt 1105
105 Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser
106 195 200 205
108 aaa gaa caa aga ctt aag gaa cag ctt ggc gct caa caa gaa cca gtg 1153
109 Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val
110 210 215 220
112 aag aaa tcc att cag gaa tca gaa gct ttt ttg cct cag agc ata cct 1201
113 Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro
114 225 230 235 240
116 gaa gag aga tac aag atg aag agc aag ccc cta gga atc tgc ctg ata 1249
117 Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile
118 245 250 255
120 atc gat tgc att ggc aat gag aca gag ctt ctt cga gac acc ttc act 1297
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122 260 265 270
124 tcc ctg ggc tat gaa gtc cag aaa ttc ttg cat ctc agt atg cat ggt 1345
125 Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly
126 275 280 285
128 ata tcc cag att ctt ggc caa ttt gcc tgt atg ccc gag cac cga gac 1393
129 Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp
130 290 295 300
132 tac gac agc ttt gtg tgt gtc ctg gtg agc cga gga ggc tcc cag agt 1441
133 Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser
134 305 310 315 320
136 gtg tat ggt gtg gat cag act cac tca ggg ctc ccc ctg cat cac atc 1489
137 Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile

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141 Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro
142          340          345          350
144 aag atg ttt ttt att cag aac tat gtg gtg tca gag ggc cag ctg gag 1585
145 Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu
146          355          360          365
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149 Asn Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu
150          370          375          380
152 ttc aag gct cag aag cga ggg ctg tgc aca gtt cac cga gaa gct gac 1681
153 Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp
154 385          390          395          400
156 ttc ttc tgg agc ctg tgt act gcg gac atg tcc ctg ctg gag cag tct 1729
157 Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser
158          405          410          415
160 cac agc tca ccg tcc ctg tac ctg cag tgc ctc tcc cag aaa ctg aga 1777
161 His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg
162          420          425          430
164 caa gaa aga aaa cgc cca ctc ctg gat ctt cac att gaa ctc aat ggc 1825
165 Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
166          435          440          445
168 tac atg tat gat tgg aac agc aga gtt tct gcc aag gag aaa tat tat 1873
169 Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr
170          450          455          460
172 gtc tgg ctg cag cac act ctg aga aag aaa ctt atc ctc tcc tac aca 1921
173 Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
174 465          470          475          480
176 taagaaacca aaaggctggg cgtagtggct cacacctgta atcccagcac tttgggaggc 1981
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198 Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
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201 Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
202 35 40 45
204 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
205 50 55 60
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208 65 70 75 80

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216 Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
217      115      120      125
219 Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
220      130      135      140
222 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
223 145      150      155      160
225 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
226      165      170      175
228 Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
229      180      185      190
231 Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser
232      195      200      205
234 Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val
235      210      215      220
237 Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro
238 225      230      235      240
240 Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile
241      245      250      255
243 Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr
244      260      265      270
246 Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly
247      275      280      285
249 Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp
250      290      295      300
252 Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser
253 305      310      315      320
255 Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile
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258 Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro
259      340      345      350
261 Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu
262      355      360      365
264 Asn Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu
265      370      375      380
267 Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp
268 385      390      395      400
270 Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser
271      405      410      415
273 His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg
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276 Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
277      435      440      445
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322 35 40 45
324 aag ctg tct gtc ggg gac ttg gct gaa ctg ctc tac aga gtg agg cga 673
325 Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
326 50 55 60
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346 130 135 140
348 gcc cca gat caa ctg gat tta tta gaa aaa tgc cta aag aac atc cac 961
349 Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
350 145 150 155 160
352 aga ata gac ctg aag aca aaa atc cag aag tac aag cag tct gtt caa 1009
353 Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln

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VERIFICATION SUMMARY

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